

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Ammons, William Steve et al.
- (ii) TITLE OF INVENTION: Method of Treating Conditions Associated with Intestinal Ischemia/Reperfusion
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY INFORMATION:
 - (A) NAME: Sharp, Jeffrey S.
 - (B) REGISTRATION NUMBER: 31,879
 - (C) REFERENCE/DOCKET NUMBER: 27129/32043
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 312/474-6300
 - (B) TELEFAX: 312/474-0448
 - (C) TELEX: 25-3856

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1813 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 31..1491
- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 124..1491

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(D) OTHER INFORMATION: "rBPI"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGGCCTTGA GGTTTTGGCA GCTCTGGAGG ATG AGA GAG AAC ATG GCC AGG GGC	54
Met Arg Glu Asn Met Ala Arg Gly	
-31 -30 -25	
CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GTG CTC GTC GCC ATA	102
Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile	
-20 -15 -10	
GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC	150
Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile	
-5 1 5	
TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG ACG GCC GCT CTG	198
Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu	
10 15 20 25	
CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT	246
Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe	
30 35 40	
AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTC TAC AGC ATG GAC	294
Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp	
45 50 55	
ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT	342
Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn	
60 65 70	
GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGC	390
Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly	
75 80 85	
AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC	438
Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp	
90 95 100 105	
CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT	486
Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser	
110 115 120	
AAC CCC ACG TCA GGC AAG CCC ACC ATC ACC TGC TCC AGC TGC AGC AGC	534
Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser	
125 130 135	
CAC ATC AAC AGT GTC CAC GTG CAC ATC TCA AAG AGC AAA GTC GGG TGG	582
His Ile Asn Ser Val His Val His Ile Ser Lys Ser Lys Val Gly Trp	
140 145 150	
CTG ATC CAA CTC TTC CAC AAA AAA ATT GAG TCT GCG CTT CGA AAC AAG	630
Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys	
155 160 165	
ATG AAC AGC CAG GTC TGC GAG AAA GTG ACC AAT TCT GTA TCC TCC AAG	678
Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Ser Lys	
170 175 180 185	
CTG CAA CCT TAT TTC CAG ACT CTG CCA GTA ATG ACC AAA ATA GAT TCT	726

Leu	Gln	Pro	Tyr	Phe 190	Gln	Thr	Leu	Pro	Val 195	Met	Thr	Lys	Ile	Asp 200	Ser	
GTG Val	GCT Ala	GGA Gly	ATC Ile 205	AAC Asn	TAT Tyr	GGT Gly	CTG Leu 210	GTG Val	GCA Ala	CCT Pro	CCA Pro	GCA Ala	ACC Thr 215	ACG Thr	GCT Ala	774
GAG Glu	ACC Thr	CTG Leu 220	GAT Asp	GTA Val	CAG Gln	ATG Met	AAG Lys 225	GGG Gly	GAG Glu	TTT Phe	TAC Tyr	AGT Ser 230	GAG Glu	AAC Asn	CAC His	822
CAC His	AAT Asn 235	CCA Pro	CCT Pro	CCC Pro	TTT Phe	GCT Ala 240	CCA Pro	CCA Pro	GTG Val	ATG Met	GAG Glu 245	TTT Phe	CCC Pro	GCT Ala	GCC Ala	870
CAT His 250	GAC Asp	CGC Arg	ATG Met	GTA Val	TAC Tyr 255	CTG Leu	GGC Gly	CTC Leu	TCA Ser	GAC Asp 260	TAC Tyr	TTC Phe	TTC Phe	AAC Asn	ACA Thr 265	918
GCC Ala	GGG Gly	CTT Leu	GTA Val	TAC Tyr 270	CAA Gln	GAG Glu	GCT Ala	GGG Gly	GTC Val 275	TTG Leu	AAG Lys	ATG Met	ACC Thr	CTT Leu 280	AGA Arg	966
GAT Asp	GAC Asp	ATG Met	ATT Ile 285	CCA Pro	AAG Lys	GAG Glu	TCC Ser	AAA Lys 290	TTT Phe	CGA Arg	CTG Leu	ACA Thr	ACC Thr 295	AAG Lys	TTC Phe	1014
TTT Phe	GGA Gly	ACC Thr 300	TTC Phe	CTA Leu	CCT Pro	GAG Glu	GTG Val 305	GCC Ala	AAG Lys	AAG Lys	TTT Phe	CCC Pro 310	AAC Asn	ATG Met	AAG Lys	1062
ATA Ile	CAG Gln 315	ATC Ile	CAT His	GTC Val	TCA Ser	GCC Ala 320	TCC Ser	ACC Thr	CCG Pro	CCA Pro	CAC His 325	CTG Leu	TCT Ser	GTG Val	CAG Gln	1110
CCC Pro 330	ACC Thr	GGC Gly	CTT Leu	ACC Thr	TTC Phe 335	TAC Tyr	CCT Pro	GCC Ala	GTG Val	GAT Asp 340	GTC Val	CAG Gln	GCC Ala	TTT Phe	GCC Ala 345	1158
GTC Val	CTC Leu	CCC Pro	AAC Asn	TCC Ser 350	TCC Ser	CTG Leu	GCT Ala	TCC Ser	CTC Leu 355	TTC Phe	CTG Leu	ATT Ile	GGC Gly	ATG Met 360	CAC His	1206
ACA Thr	ACT Thr	GGT Gly	TCC Ser 365	ATG Met	GAG Glu	GTC Val	AGC Ser	GCC Ala 370	GAG Glu	TCC Ser	AAC Asn	AGG Arg	CTT Leu 375	GTT Val	GGA Gly	1254
GAG Glu	CTC Leu	AAG Lys 380	CTG Leu	GAT Asp	AGG Arg	CTG Leu	CTC Leu 385	CTG Leu	GAA Glu	CTG Leu	AAG Lys	CAC His 390	TCA Ser	AAT Asn	ATT Ile	1302
GGC Gly	CCC Pro 395	TTC Phe	CCG Pro	GTT Val	GAA Glu	TTG Leu 400	CTG Leu	CAG Gln	GAT Asp	ATC Ile	ATG Met 405	AAC Asn	TAC Tyr	ATT Ile	GTA Val	1350
CCC Pro 410	ATT Ile	CTT Leu	GTG Val	CTG Leu	CCC Pro 415	AGG Arg	GTT Val	AAC Asn	GAG Glu	AAA Lys 420	CTA Leu	CAG Gln	AAA Lys	GGC Gly	TTC Phe 425	1398
CCT Pro	CTC Leu	CCG Pro	ACG Thr	CCG Pro 430	GCC Ala	AGA Arg	GTC Val	CAG Gln	CTC Leu 435	TAC Tyr	AAC Asn	GTA Val	GTG Val	CTT Leu 440	CAG Gln	1446
CCT Pro	CAC His	CAG Gln	AAC Asn	TTC Phe	CTG Leu	CTG Leu	TTC Phe	GGT Gly	GCA Ala	GAC Asp	GTT Val	GTC Val	TAT Tyr	AAA Lys		1491

445	450	455	
TGAAGGCACC	AGGGGTGCCG	GGGGCTGTCA	GCCGCACCTG TTCCTGATGG GCTGTGGGGC 1551
ACCGGCTGCC	TTTCCCCAGG	GAATCCTCTC	CAGATCTTAA CCAAGAGCCC CTTGCAAAC 1611
TCTTCGACTC	AGATTCAGAA	ATGATCTAAA	CACGAGGAAA CATTATTCAT TGGAAAAGTG 1671
CATGGTGTGT	ATTTTAGGGA	TTATGAGCTT	CTTTCAAGGG CTAAGGCTGC AGAGATATTT 1731
CCTCCAGGAA	TCGTGTTTCA	ATTGTAACCA	AGAAATTTC ATTTGTGCTT CATGAAAAA 1791
AACTTCTGGT	TTTTTTCATG	TG	1813

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Arg	Glu	Asn	Met	Ala	Arg	Gly	Pro	Cys	Asn	Ala	Pro	Arg	Trp	Val	-31	-30	-25	-20
Ser	Leu	Met	Val	Leu	Val	Ala	Ile	Gly	Thr	Ala	Val	Thr	Ala	Ala	Val	-15	-10	-5	1
Asn	Pro	Gly	Val	Val	Val	Arg	Ile	Ser	Gln	Lys	Gly	Leu	Asp	Tyr	Ala	5	10	15	
Ser	Gln	Gln	Gly	Thr	Ala	Ala	Leu	Gln	Lys	Glu	Leu	Lys	Arg	Ile	Lys	20	25	30	
Ile	Pro	Asp	Tyr	Ser	Asp	Ser	Phe	Lys	Ile	Lys	His	Leu	Gly	Lys	Gly	35	40	45	
His	Tyr	Ser	Phe	Tyr	Ser	Met	Asp	Ile	Arg	Glu	Phe	Gln	Leu	Pro	Ser	50	55	60	65
Ser	Gln	Ile	Ser	Met	Val	Pro	Asn	Val	Gly	Leu	Lys	Phe	Ser	Ile	Ser	70	75	80	
Asn	Ala	Asn	Ile	Lys	Ile	Ser	Gly	Lys	Trp	Lys	Ala	Gln	Lys	Arg	Phe	85	90	95	
Leu	Lys	Met	Ser	Gly	Asn	Phe	Asp	Leu	Ser	Ile	Glu	Gly	Met	Ser	Ile	100	105	110	
Ser	Ala	Asp	Leu	Lys	Leu	Gly	Ser	Asn	Pro	Thr	Ser	Gly	Lys	Pro	Thr	115	120	125	
Ile	Thr	Cys	Ser	Ser	Cys	Ser	Ser	His	Ile	Asn	Ser	Val	His	Val	His	130	135	140	145
Ile	S	r	Lys	Ser	Lys	Val	Gly	Trp	Leu	Ile	Gln	Leu	Phe	His	Lys	150	155	160	
Ile	Glu	Ser	Ala	Leu	Arg	Asn	Lys	Met	Asn	Ser	Gln	Val	Cys	Glu	Lys	165	170	175	

[illegible]